

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: BECKMANN, M. P.  
CERRETTI, DOUGLAS P.
- (ii) TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
RECEPTOR HEK
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: IMMUNEX CORPORATION  
(B) STREET: 51 UNIVERSITY STREET  
(C) CITY: SEATTLE  
(D) STATE: WASHINGTON  
(E) COUNTRY: USA  
(F) ZIP: 98101
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: Apple Macintosh  
(C) OPERATING SYSTEM: Apple System 7.1  
(D) SOFTWARE: Microsoft Word for Apple, Version 5.1a
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/161,132  
(B) FILING DATE: 03-DEC-1993
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/114,426  
(B) FILING DATE: 30-AUG-1993
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/109,745  
(B) FILING DATE: 20-AUG-1993
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: SEESE, KATHRYN A.  
(B) REGISTRATION NUMBER: 32,172  
(C) REFERENCE/DOCKET NUMBER: 2814-C
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (206) 587-0430  
(B) TELEFAX: (206) 233-0644  
(C) TELEX: 756822

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1037 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: hek-L A2

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 83..799

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 83..139

(ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 140..796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATCTTGA ACGAGACGAC CTGCTGGAGA AGCCGGGAGC GCGGGGCTCA GTCGGGGGGC	60
GGCGGCGGCG GCGGCTCCGG GG ATG GCG GCG GCT CCG CTG CTG CTG CTG CTG	112
Met Ala Ala Ala Pro Leu Leu Leu Leu Leu	
-19 -15 -10	
CTG CTC GTG CCC GTG CCG CTG CTG CCG CTG CTG GCC CAA GGG CCC GGA	160
Leu Leu Val Pro Val Pro Leu Leu Pro Leu Leu Ala Gln Gly Pro Gly	
-5 1 5	
GGG GCG CTG GGA AAC CGG CAT GCG GTG TAC TGG AAC AGC TCC AAC CAG	208
Gly Ala Leu Gly Asn Arg His Ala Val Tyr Trp Asn Ser Ser Asn Gln	
10 15 20	
CAC CTG CGG CGA GAG GGC TAC ACC GTG CAG GTG AAC GTG AAC GAC TAT	256
His Leu Arg Arg Glu Gly Tyr Thr Val Gln Val Asn Val Asn Asp Tyr	
25 30 35	
CTG GAT ATT TAC TGC CCG CAC TAC AAC AGC TCG GGG GTG GGC CCC GGG	304
Leu Asp Ile Tyr Cys Pro His Tyr Asn Ser Ser Gly Val Gly Pro Gly	
40 45 50 55	
GCG GGA CCG GGG CCC GGA GGC GGG GCA GAG CAG TAC GTG CTG TAC ATG	352
Ala Gly Pro Gly Pro Gly Gly Gly Ala Glu Gln Tyr Val Leu Tyr Met	
60 65 70	

GTG AGC CGC AAC GGC TAC CGC ACC TGC AAC GCC AGC CAG GGC TTC AAG 400  
 Val Ser Arg Asn Gly Tyr Arg Thr Cys Asn Ala Ser Gln Gly Phe Lys  
 75 80 85  
 CGC TGG GAG TGC AAC CGG CCG CAC GCC CCG CAC AGC CCC ATC AAG TTC 448  
 Arg Trp Glu Cys Asn Arg Pro His Ala Pro His Ser Pro Ile Lys Phe  
 90 95 100  
 TCG GAG AAG TTC CAG CGC TAC AGC GCC TTC TCT CTG GGC TAC GAG TTC 496  
 Ser Glu Lys Phe Gln Arg Tyr Ser Ala Phe Ser Leu Gly Tyr Glu Phe  
 105 110 115  
 CAC GCC GGC CAC GAG TAC TAC TAC ATC TCC ACG CCC ACT CAC AAC CTG 544  
 His Ala Gly His Glu Tyr Tyr Tyr Ile Ser Thr Pro Thr His Asn Leu  
 120 125 130 135  
 CAC TGG AAG TGT CTG AGG ATG AAG GTG TTC GTC TGC TGC GCC TCC ACA 592  
 His Trp Lys Cys Leu Arg Met Lys Val Phe Val Cys Cys Ala Ser Thr  
 140 145 150  
 TCG CAC TCC GGG GAG AAG CCG GTC CCC ACT CTC CCC CAG TTC ACC ATG 640  
 Ser His Ser Gly Glu Lys Pro Val Pro Thr Leu Pro Gln Phe Thr Met  
 155 160 165  
 GGC CCC AAT GTG AAG ATC AAC GTG CTG GAA GAC TTT GAG GGA GAG AAC 688  
 Gly Pro Asn Val Lys Ile Asn Val Leu Glu Asp Phe Glu Gly Glu Asn  
 170 175 180  
 CCT CAG GTG CCC AAG CTT GAG AAG AGC ATC AGC GGG ACC AGC CCC AAA 736  
 Pro Gln Val Pro Lys Leu Glu Lys Ser Ile Ser Gly Thr Ser Pro Lys  
 185 190 195  
 CGG GAA CAC CTG CCC CTG GCC GTG GGC ATC GCC TTC TTC CTC ATG ACG 784  
 Arg Glu His Leu Pro Leu Ala Val Gly Ile Ala Phe Phe Leu Met Thr  
 200 205 210 215  
 TTC TTG GCC TCC TAGCTCTGCC CCCTCCCCTG EGGGGGGGAGA GATGGGGCGG 836  
 Phe Leu Ala Ser  
 220  
 GGCTTGAAG GAGCAGGGAG CCTTTGGCCT CTCCAAGGGA AGCCTAGTGG GCCTAGACCC 896  
 CTCCTCCCAT GGCTAGAAGT GGGGCCTGCA CCATACATCT GTGTCCGCCC CCTCTACCCC 956  
 TTCCCCCACC GTAGGGCACT GTAGTGGACC AAGCACGGGG ACAGCCATGG GTCCCGAGCA 1016  
 GGTCGTCTCG TTCCAAGATC C 1037

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ala Ala Pro Leu Leu Leu Leu Leu Leu Val Pro Val Pro  
 -19 -15 -10 -5

Leu Leu Pro Leu Leu Ala Gln Gly Pro Gly Gly Ala Leu Gly Asn Arg  
 1 5 10

His Ala Val Tyr Trp Asn Ser Ser Asn Gln His Leu Arg Arg Glu Gly  
 15 20 25

Tyr Thr Val Gln Val Asn Val Asn Asp Tyr Leu Asp Ile Tyr Cys Pro  
 30 35 40 45

His Tyr Asn Ser Ser Gly Val Gly Pro Gly Ala Gly Pro Gly Pro Gly  
 50 55 60

Gly Gly Ala Glu Gln Tyr Val Leu Tyr Met Val Ser Arg Asn Gly Tyr  
 65 70 75

Arg Thr Cys Asn Ala Ser Gln Gly Phe Lys Arg Trp Glu Cys Asn Arg  
 80 85 90

Pro His Ala Pro His Ser Pro Ile Lys Phe Ser Glu Lys Phe Gln Arg  
 95 100 105

Tyr Ser Ala Phe Ser Leu Gly Tyr Glu Phe His Ala Gly His Glu Tyr  
 110 115 120 125

Tyr Tyr Ile Ser Thr Pro Thr His Asn Leu His Trp Lys Cys Leu Arg  
 130 135 140

Met Lys Val Phe Val Cys Cys Ala Ser Thr Ser His Ser Gly Glu Lys  
 145 150 155

Pro Val Pro Thr Leu Pro Gln Phe Thr Met Gly Pro Asn Val Lys Ile  
 160 165 170

Asn Val Leu Glu Asp Phe Glu Gly Glu Asn Pro Gln Val Pro Lys Leu  
 175 180 185

Glu Lys Ser Ile Ser Gly Thr Ser Pro Lys Arg Glu His Leu Pro Leu  
 190 195 200 205

Ala Val Gly Ile Ala Phe Phe Leu Met Thr Phe Leu Ala Ser  
 210 215

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: hek-L C6

(ix) FEATURE:  
(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 94..630

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 28..633

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 28..93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCAGACCAA ACCGGACCTC GGGGGCG ATG CGG CTG CTG CCC CTG CTG CGG	51
Met Arg Leu Leu Pro Leu Leu Arg	
-22 -20 -15	
ACT GTC CTC TGG GCC GCG TTC CTC GGC TCC CCT CTG CGC GGG GGC TCC	99
Thr Val Leu Trp Ala Ala Phe Leu Gly Ser Pro Leu Arg Gly Gly Ser	
-10 -5 1	
AGC CTC CGC CAC GTA GTC TAC TGG AAC TCC AGT AAC CCC AGG TTG CTT	147
Ser Leu Arg His Val Val Tyr Trp Asn Ser Ser Asn Pro Arg Leu Leu	
5 10 15	
CGA GGA GAC GCC GTG GTG GAG CTG GGC CTC AAC GAT TAC CTA GAC ATT	195
Arg Gly Asp Ala Val Val Glu Leu Gly Leu Asn Asp Tyr Leu Asp Ile	
20 25 30	
GTC TGC CCC CAC TAC GAA GGC CCA GGG CCC CCT GAG GGC CCC GAG ACG	243
Val Cys Pro His Tyr Glu Gly Pro Gly Pro Pro Glu Gly Pro Glu Thr	
35 40 45 50	
TTT GCT TTG TAC ATG GTG GAC TGG CCA GGC TAT GAG TCC TGC CAG GCA	291
Phe Ala Leu Tyr Met Val Asp Trp Pro Gly Tyr Glu Ser Cys Gln Ala	
55 60 65	
GAG GGC CCC CGG GCC TAC AAG CGC TGG GTG TGC TCC CTG CCC TTT GGC	339
Glu Gly Pro Arg Ala Tyr Lys Arg Trp Val Cys Ser Leu Pro Phe Gly	
70 75 80	
CAT GTT CAA TTC TCA GAG AAG ATT CAG CGC TTC ACA CCT TTC TCC CTC	387
His Val Gln Phe Ser Glu Lys Ile Gln Arg Phe Thr Pro Phe Ser Leu	
85 90 95	
GGC TTT GAG TTC TTA CCT GGA GAG ACT TAC TAC TAC ATC TCG GTG CCC	435
Gly Phe Glu Phe Leu Pro Gly Glu Thr Tyr Tyr Tyr Ile Ser Val Pro	
100 105 110	
ACT CCA GAG AGT TCT GGC CAG TGC TTG AGG CTC CAG GTG TCT GTC TGC	483
Thr Pro Glu Ser Ser Gly Gln Cys Leu Arg Leu Gln Val Ser Val Cys	
115 120 125 130	

TGC AAG GAG AGG AAG TCT GAG TCA GCC CAT CCT GTT GGG AGC CCT GGA 531  
 Cys Lys Glu Arg Lys Ser Glu Ser Ala His Pro Val Gly Ser Pro Gly  
 135 140 145  
 GAG AGT GGC ACA TCA GGG TGG CGA GGG GGG GAC ACT CCC AGC CCC CTC 579  
 Glu Ser Gly Thr Ser Gly Trp Arg Gly Gly Asp Thr Pro Ser Pro Leu  
 150 155 160  
 TGT CTC TTG CTA TTA CTG CTG CTT CTG ATT CTT CGT CTT CTG CGA ATT 627  
 Cys Leu Leu Leu Leu Leu Leu Leu Leu Ile Leu Arg Leu Leu Arg Ile  
 165 170 175  
 CTG TGAGCC 636  
 Leu  
 180

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Leu Leu Pro Leu Leu Arg Thr Val Leu Trp Ala Ala Phe Leu  
 -22 -20 -15 -10  
 Gly Ser Pro Leu Arg Gly Gly Ser Ser Leu Arg His Val Val Tyr Trp  
 -5 1 5 10  
 Asn Ser Ser Asn Pro Arg Leu Leu Arg Gly Asp Ala Val Val Glu Leu  
 15 20 25  
 Gly Leu Asn Asp Tyr Leu Asp Ile Val Cys Pro His Tyr Glu Gly Pro  
 30 35 40  
 Gly Pro Pro Glu Gly Pro Glu Thr Phe Ala Leu Tyr Met Val Asp Trp  
 45 50 55  
 Pro Gly Tyr Glu Ser Cys Gln Ala Glu Gly Pro Arg Ala Tyr Lys Arg  
 60 65 70  
 Trp Val Cys Ser Leu Pro Phe Gly His Val Gln Phe Ser Glu Lys Ile  
 75 80 85 90  
 Gln Arg Phe Thr Pro Phe Ser Leu Gly Phe Glu Phe Leu Pro Gly Glu  
 95 100 105  
 Thr Tyr Tyr Tyr Ile Ser Val Pro Thr Pro Glu Ser Ser Gly Gln Cys  
 110 115 120  
 Leu Arg Leu Gln Val Ser Val Cys Lys Glu Arg Lys Ser Glu Ser  
 125 130 135

Ala His Pro Val Gly Ser Pro Gly Glu Ser Gly Thr Ser Gly Trp Arg  
 140 145 150

Gly Gly Asp Thr Pro Ser Pro Leu Cys Leu Leu Leu Leu Leu Leu  
 155 160 165 170

Leu Ile Leu Arg Leu Leu Arg Ile Leu  
 175

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